

58. The method as claimed in claim 30, wherein the DNA fragment is at least 90% homologous to the corresponding nucleotide sequence of the genomic RNA 1 of said virus.

59. The method as claimed in claim 30, wherein the DNA fragment is at least 95% homologous to the corresponding nucleotide sequence of the genomic RNA 1 of said virus.

60. The vector as claimed in claim 38, wherein the fragment is at least 90% homologous to the corresponding nucleotide sequence of the genomic RNA 1 of said virus.

61. The vector as claimed in claim 38, wherein the fragment is at least 95% homologous to the corresponding nucleotide sequence of the genomic RNA 1 of said virus.

IN THE ABSTRACT:

After the claims, please insert a page containing the Abstract Of The Disclosure, which is attached hereto as a separately typed page.

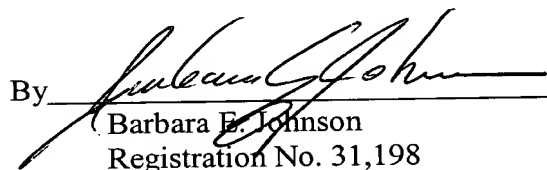
REMARKS

The specification has been amended to place the application in conformance with standard United States patent practice.

Examination and allowance of pending claims 30-61 are respectfully
requested.

Respectfully submitted,

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MARKED-UP AMENDED SPECIFICATION PARAGRAPHS

Paragraph bridging pages 4 and 5

The homology or "degree of similarity" is used to denote nucleotide sequences which when aligned have similar (identical or conservatively replaced) nucleotides in like positions or regions. For example, two nucleotide sequences with at least 85% homology to each other have at least 85% homologous (identical or conservatively replaced nucleotides) in a like position when aligned optimally allowing for up to 3 gaps, with the [provison] provision that in respect of the gaps a total of not more than 15 amino acid [resides] residues is affected. The degree of similarity may be determined using methods well known in the art (see, for example, Wilbur, W.J. and Lipman, D.J. "Rapid Similarity Searches of Nucleic Acid and Protein Data Banks." Proceedings of the National Academy of Sciences USA 80, 726-730 (1983) and Myers E. and Miller W. "Optimal Alignments in Linear Space". Comput. Appl. Biosci. 4:11-17(1988)). One programme which may be used in determining the degree of similarity is the MegAlign Lipman-Pearson one pair method (using default parameters) which can be obtained from DNASTAR Inc, 1228, Selfpark Street, Madison, Wisconsin, 53715, USA as part of the Lasergene system. The test for homology of the sequence is based on the percent identity which is calculated by Fast DB based on the following parameters: mismatch penalty 1.0, gap penalty (1.00), gap size penalty 0.33 and joining penalty 30.0.

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Figure 4 shows diagrams of the individual ELISA values of the root extracts of sugar beet plants of the populations Cadyx [(susceptibel] (susceptible control), Rifle (rhizomania tolerant variety), Rhizor (rhizomania tolerant variety) and

T157-01 (GUS-positive F1 individuals) after inoculation with BNYVV-infested soil.

Each number at the horizontal axis represents an individual plant.